Serial No.: 10/552,857

Response to Office Action mailed: June 28, 2011

Amendment Dated: August 29, 2011

## REMARKS/ARGUMENTS

This is in response to the Office Action mailed June 28, 2011 for the above-captioned application.

Claims 98-102 were indicated as allowed.

Claims 83-97 were rejected. Without conceding the merits of the rejection, Applicants have now amended these claims to delete references to variants and deleted claims 85-88 consistent with this amendment. This amendment is believed to overcome the rejection of these claims which was based on the enablement and written description requirements of 35 USC § 112, first paragraph, and applied only to variants.

It is also noted that in ¶ 8 of the office action, the Examiner withdrew the restriction requirement with respect to Seq ID Nos. 12, 14 and 16.

Final reconsideration and clarification of the restriction requirement with respect to the claims of this application which are believed by Applicants to be allowable is requested. No art has been cited in this application that would render a construct of the type claimed unpatentable. Thus, the generic concept of the invention is patentable over the art, independent of the specific sequences employed.

Claims 98-102, which include sequences including all of the specific sequences options are allowed, yet the examiner states that cancellation of non-elected sequences is required. This makes the position on the restriction of sequences underclear.

Claim 83 and allowed claim 98 each recite four options for the CHS part of the construct, as either the nucleotide sequence or the peptide encoded, and one option for the anthocyanine reductase as either the nucleic acid sequence or the peptide encoded. The four CHS peptide sequences (2, 4, 6 and 8) were shown in the alignment filed as Appendix A of the response dated August 18, 2010 to have a relatively high level of sequence similarity. As previously noted, in this Table, the sequences correspond to seq ID Nos. 2, 4, 6, and 8, respectively. For convenient consideration, the relevant part of this Appendix (the CHS amino acid alignment) is again attached. Combined with the common function, Applicants submit that in this circumstance it is not in the public interest to have four separate patents issued with such similar subject matter claimed.

It is noted further that within the non-elected peptide sequences, the level of similarity between Seq ID No 8 and elected seq ID No. 2 is particularly high. Thus, at a minimum,

Serial No.: 10/552,857

Response to Office Action mailed: June 28, 2011

Amendment Dated: August 29, 2011

Applicants submit that Seq ID No 8, and corresponding nucleotide sequence 7 should be recombined.

Applicants submit that all claims of this application are now appropriately allowed without further amendments and such action is respectfully urged. Should the Examiner wish to discuss this matter, she is invited to contact the undersigned by telephone.

Respectfully submitted,

Marina T. Larson, Ph.D

Attorney/Agent for Applicant(s)

Marina I La

Reg. No. 32038

(970) 262-1800

## TrCHS amino acid sequence alignment

| ~16  | 162. | TrCHS3ap                                   | :        | MVSVAETRKAORAEGPATIDATGTANEPNRVEOSTYPDFYEKITNSEEKTED   |          |
|------|------|--|----------|--|----------|
|      | 102  | : 52<br>TrCHScp                            | :        | MGDEGIVREVTKQTTPGKATILALGKAFPHOLVMOEGEVDGYERDTNGDN-PEL   |          |
|      | 104  | : 53<br>TrCHSfp                            | :        | -NPOGDINGSSSVNGARARRAPTOGKATILATGKATPAQVIPOECTVEGEIRDTKEDD-TYI   |          |
| Seq  | 106  | : 60                                       |          | MVINE IRNAGRSNGPATILAFGTATESNCVTQADYPDYYERITNSEHMTDL   |          |
| sey. | 100  | TrCHShp<br>: 52                            | •        |  |          |
|      |      | TrCHS3ap                                   | :        | KEKEORMCDKSMIKSRYMYLTEETIKENPSLEEMAESLDARODMWVWEVERLGKEAAV 201   |          |
|      |      | : 114<br>TrCHScp                           | :        | KOKLARLOKTTTVKTRYVVMNEETILKKYPELVVEGASTVKORTEICTEAVTOMAIGASQVOL  |          |
|      |      | : 115<br>TrCHSfp                           | ;        | KEKLERLCKNTTVKKRYTVMSKETLDNYPELAIDETETIROKTEIAKPAVVEMATRASKDCI   |          |
|      |      | : 122<br>TrCHShp                           | :        | KEKEKRMCDRSMIKKRYMHLTEDFLKENPNMCEMMAESLDVRRDIVVWEVEKLGGEAAKKAI   |          |
|      |      | : 114                                      |          |  |          |
|      |      | TrCHS3ap                                   | :        | ĸewgorks <mark>k</mark> ithlifetts <mark>e</mark> vompgadyoltkolgi <mark>rpyvkry</mark> mmyoogcfaggtvilrlakd   |          |
|      |      | : 176<br>TrCHScp                           | :        | KNWGRSISBITHVVYVSSSBARLPGGDBYLGKGLGLNPKIQRTMLYBSGCSGGVAGLRVAKD   | 1        |
|      |      | : 177<br>TrCHSfp                           | :        | KEWGRSPONTHIVY <mark>VSSSNIRLPGGDNYLANELGLNSDVNR</mark> MLYNLGCYG <mark>GV</mark> TGLRVAKD   |          |
|      |      | : 184<br>TrCHShp                           | . :      | CEWG REMMY Q GCERGET VELAKD  | 1        |
|      |      | : 176                                      |          |  | <b>រ</b> |
|      | •    | TrCHS3ar<br>: 238                          | :        | LAENNKGARVLVVOSE <mark>VTAVT</mark> FREPSDINHIDSLVGQALFGDGAAATIVGSDPV <mark>PEHEK</mark> PITE  |          |
| •    |      | TrCHScp: 239                               | :        | VAENNPGSRVLLATSENTIIEFKPPSVDRPYNLVG <mark>V</mark> ALFGDGA <mark>G</mark> AMIIGSDPVENTENPLEE   |          |
|      |      | TrCHSfp: 246                               | ;        | IAENNPGSRVILTTSEETILGFRPPSKARPYTLVGAALFGDGAAAAIIGTDPIENQESPFM  |          |
|      |      | TrCHShp: 238                               | . :      | LVENNKNARVLVVOSE <mark>ITAVT</mark> FREPSDIERDSLVGEALFGDGAAAMIIG <mark>A</mark> DPDITVERPIER   | 2        |
|      |      | -  |          | : MWTAQUIAPDSEGAIDGELEEAGLEEELEKDVPGIVSKNINKALWEAEQELGISDYNS   | Ī.       |
|      |      | TrCHS3a]<br>: 298                          |          | : LHESACE TPDTEKKIDGRETERGISET LARELEQUIEDNVEGEGNKLIDVVGLENKEYNK   |          |
|      |      | TrCHScp<br>: 301                           |          | : PHRS NO WILD DESKRIDGE TO STATE OF THE STA |          |
| •    |      | TrCHSfp<br>: 306                           |          | : LNHAVOKATIPDTONVIDGRITEEGINEKLGRDLPOKIBANIEEEGKKIMAKSDVKEFND   |          |
|      |      | TrCHShp<br>: 298                           |          | : INSTAOTITEDSDEATDGELREVGLIERLEKDVPGIISKNIERSLVEAFARIGINDWNS  |          |
|      |      | TrCHS3a                                    | מ        | : FWIAHPGGPAILDOVEOKLALKOEKMRATREVLSEYGNMSSEGVIFILDEMRKKSAONGEK  |          |
|      |      | : 360<br>TrCHScr                           |          | : FWAVHPGGPAILNRVEKRLELSBOKLNASRKALNDYGNASSNTIVYVLEYMLEEEKKI-KK  |          |
|      |      | : 362                                      |          | : FWZYHPGGPAILNKLENILKLKSDKLDCSRKALYDYGNVSSNTIFYVMEYMRDYLK   | -E       |
|      |      | TrCHSfr<br>: 363                           |          | : EWVAHPGGPAILDOVERKLHLKEEKLRSTRHVLSEYGNMSSACVLFILDOMRKRSKEEGM   | Ŀ        |
| :    |      | TrCHShp                                    | )        | : EWVMHPGGPATTLOWV DMATTALANDIA TANTV DDD OS 100 MATTALANDIA TANTV DDD OS  | ,        |
|      |      | TrCHS3                                     | ар       | : IGEGLOWGVLEGEGPGLTIETVVLRSVAL : 389  |          |
|      | 7    | TrCHSc <sub>]</sub><br>TrCHSf <sub>]</sub> | <u>ာ</u> | : TGEGLDWGVIEGEGPGLTIBTVVLRSVAH : 389<br>: GGGDSEWGLILAFGPGITECGILARNLCA : 391<br>: -DGSERWGLGLAFGPGITECGVLURSL : 389  |          |
|      |      | TrCHSh                                     |          | : REFERENCYLEGEGEGEGITVETVVLHSVPVQG : 391  |          |
|      |      |  |          |  |          |